Fig. S1 The inferred membership of 88 human individuals in *K*=3 populations by Structure. Each individual was genotyped at 783 microsatellites. The results were obtained from Structure using a burn-in length and a run length of 10^4 iterations, the admixture and correlated allele frequency models, the default (upper panel) or the alternative (lower panel) ancestry prior, and all other parameters at default values. Each individual is represented by a thin line partitioned into *K* coloured segments that represent the individual's estimated membership fractions in *K* populations.
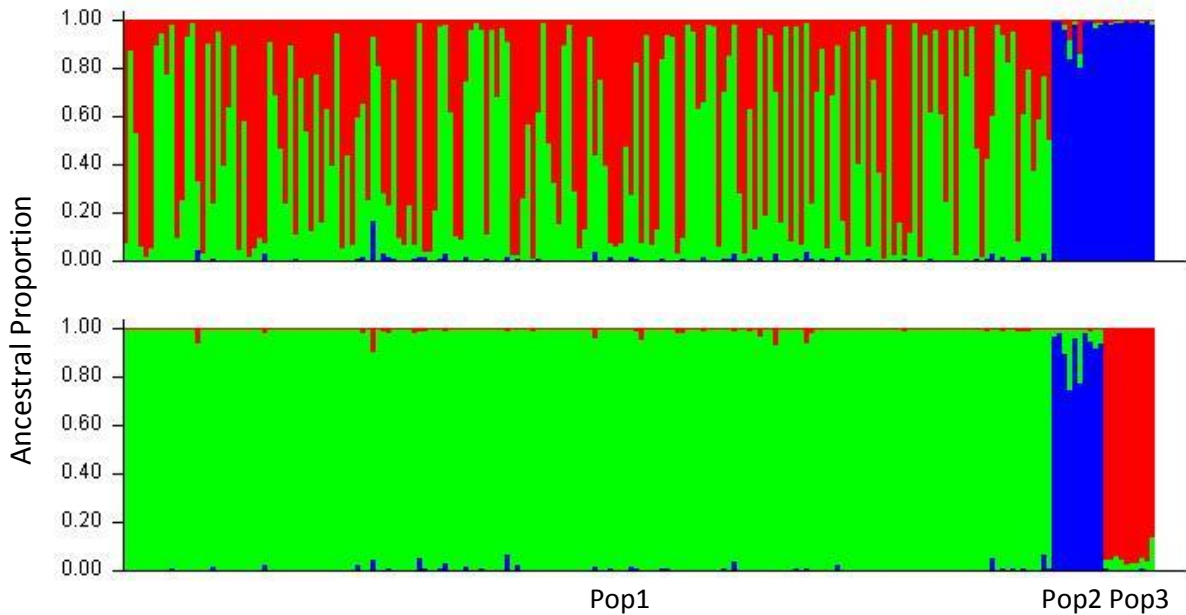
Fig. S2 The inferred membership of individuals in an example simulated dataset by Structure. The dataset has 200 simulated individuals drawn from $K=3$ populations in the island model at drift-migration-mutation equilibrium with $F_{ST}=0.10$. Individuals 1~180, 181~190, and 191~200 (ordered from left to right on the x axis) were sampled from populations 1, 2, and 3, respectively, and each individual was genotyped at 40 loci with each having 10 alleles. The analysis results were obtained from Structure using a burn-in length and a run length of 10^4 iterations, the admixture and correlated allele frequency models, the default (upper panel) or the alternative (lower panel) ancestry prior, and all other parameters at default values. Each individual (on the x axis) is represented by a thin line partitioned into $K=3$ coloured segments that represent the individual's estimated membership fractions in K populations.
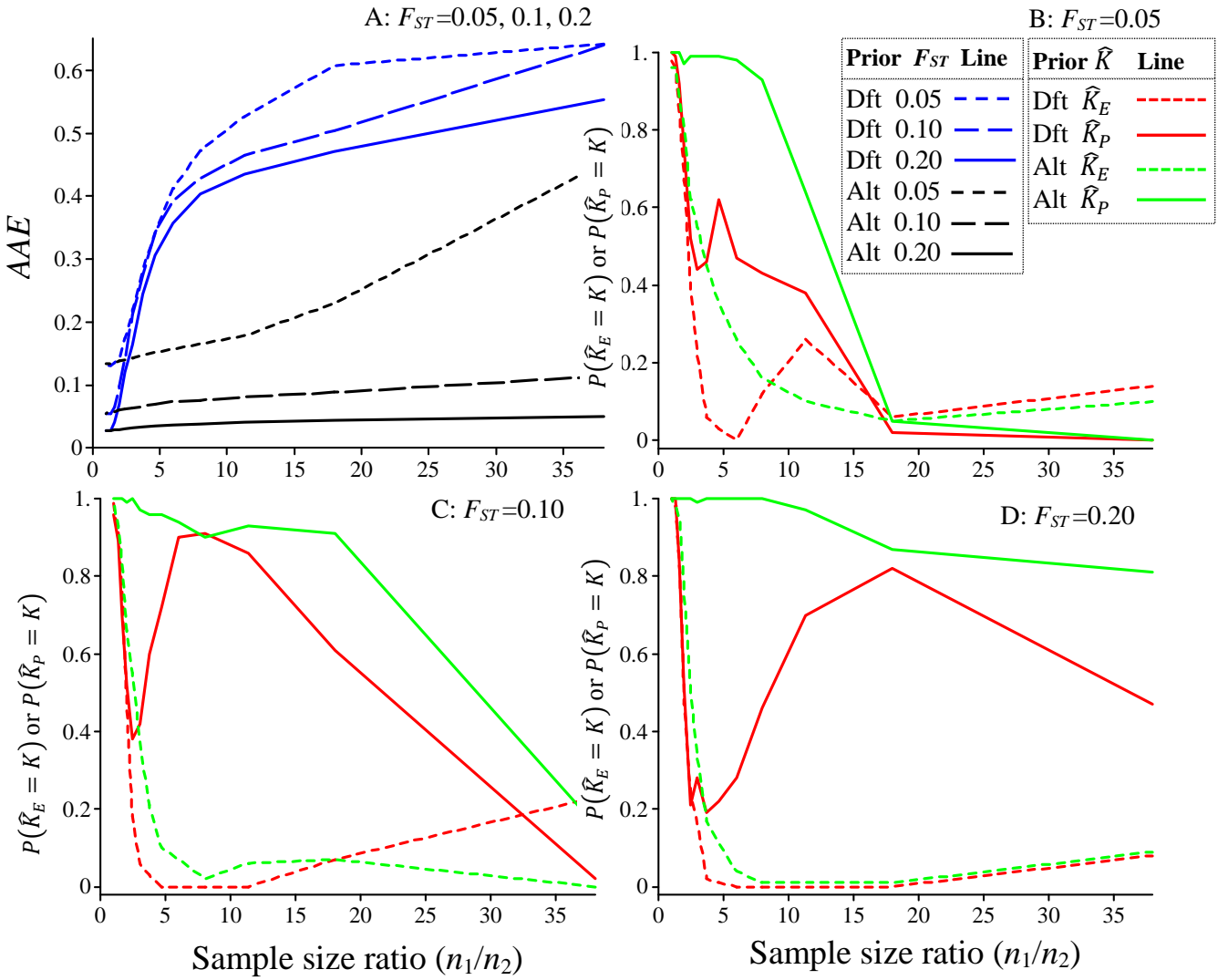
Fig. S3 Quality of individual assignments to populations and inferences of K by Structure. Three equally differentiated populations ($K=3$) with $F_{ST}=0.05$, 0.10 or 0.20 in the island model were simulated. Each individual has genotypes at $L=20$ loci, each having 10 alleles. The sample size was n_i for population i ($i=1, 2, 3$), with $n_2 \equiv n_3$ and $n_1 + n_2 + n_3 \equiv 200$. At each F_{ST} value, 100 replicate datasets were analysed by Structure using the default (Dft) and alternative (Alt) priors. The inference quality was measured by average assignment errors (AAE) in panel A, and by $P(\widehat{K}_E = K)$ and $P(\widehat{K}_P = K)$ in panels B, C, and D, as a function of the extent of unbalanced sampling measured by the sample size ratio, n_1/n_2 (x axis). A burn-in and run length of 10^4, the admixture and correlated allele frequency models, and the default values of other parameters were used in Structure analyses.
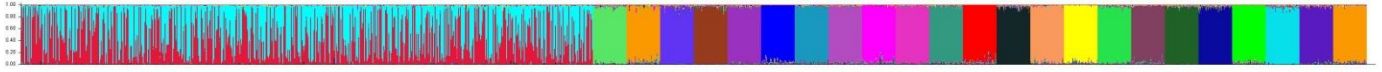
Fig. S4 The inferred membership of an example simulated dataset of 1600 individuals from K=24 populations by Structure. Individuals 1~680, 681~720, 721~760, …, 1561~1600 (ordered from left to right on x axis) were sampled from populations 1, 2, 3, …, 24 respectively, the sample size being 680 for the first population, and 40 for each of the other 23 populations. Each individual was genotyped at 50 loci with each having 10 alleles. The populations were at drift-migration-mutation equilibrium with F_{ST}=0.20. The analysis results were obtained from Structure using a burn-in length 5×10^5 and a run length 10^4 iterations, the admixture and correlated allele frequency models, the default or the alternative ancestry prior, and all other parameters at default values. Each individual (on the x axis) is represented by a thin line partitioned into K=24 coloured segments that represent the individual's estimated membership fractions in K populations.